



SEQUENCE LISTING

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(1) GENERAL INFORMATION:

- (i) APPLICANT: Tripp, Cynthia A.
Frank, Glenn R.
Grieve, Robert B.
- (ii) TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
P22U PROTEINS
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sheridan Ross P.C.
 - (B) STREET: 1700 Lincoln St., Suite 3500
 - (C) CITY: Denver
 - (D) STATE: CO
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 80203
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/460,428
 - (B) FILING DATE: 02-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Connell, Gary J.
 - (B) REGISTRATION NUMBER: 32,020
 - (C) REFERENCE/DOCKET NUMBER: 2618-13-3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 303/863-9700
 - (B) TELEFAX: 303/863-0223

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 913 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..911
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GC GAG TTA AAT AGT CGA ATT TCC GGA GTA CAC CGT AAT ACT GCA GGT

	Glu 1	Leu	Asn	Ser	Arg 5	Ile	Ser	Gly	Val	His 10	Arg	Asn	Thr	Ala	Gly 15
GCT 95	TTA	CAA	CGA	TTT	GCT	CTA	AAT	GGT	CAA	AAT	ACT	CTT	AAC	GAA	GGA
Ala	Leu	Gln	Arg	Phe 20	Ala	Leu	Asn	Gly	Gln 25	Asn	Thr	Leu	Asn	Glu 30	Gly
TCA 143	AGT	TAT	GAG	CCA	AAC	GGA	CTA	TTT	GTA	TTT	TCA	GCA	ATA	AAC	GGT
Ser	Ser	Tyr	Glu 35	Pro	Asn	Gly	Leu	Phe 40	Val	Phe	Ser	Ala	Ile 45	Asn	Gly
AGC 191	CAT	ACT	GAT	AGC	TTA	TCT	CAG	TAT	GGT	GAA	GGA	ATA	AAT	GAA	AAT
Ser	His	Thr 50	Asp	Ser	Leu	Ser	Gln 55	Tyr	Gly	Glu	Gly	Ile 60	Asn	Glu	Asn
TAT 239	CAT	TCT	GGA	ACT	AAT	TAT	TAT	GAT	GAA	GTA	GAA	TTA	AGA	GAT	AAA
Tyr	His 65	Ser	Gly	Thr	Asn	Tyr 70	Tyr	Asp	Glu	Val	Glu 75	Leu	Arg	Asp	Lys
ACA 287	AAT	CAG	ACA	TCG	TAC	ATT	AAT	GGA	AAT	GAT	AAT	GGA	ATC	AAT	GGA
Thr 80	Asn	Gln	Thr	Ser	Tyr 85	Ile	Asn	Gly	Asn	Asp 90	Asn	Gly	Ile	Asn	Gly 95
AAG 335	GAT	GAT	GAA	GAT	CTG	GAT	GAA	TGC	TCT	GAT	CAA	GAA	TTC	CGA	TGT
Lys	Asp	Asp	Glu	Asp 100	Leu	Asp	Glu	Cys	Ser 105	Asp	Gln	Glu	Phe	Arg 110	Cys
CCA 383	TAT	CTA	GCT	AAA	ACA	CTT	TGT	GTT	CAT	TAT	TTG	AAA	ATA	TGC	GAT
Pro	Tyr	Leu	Ala 115	Lys	Thr	Leu	Cys	Val 120	His	Tyr	Leu	Lys	Ile 125	Cys	Asp
GGT 431	ATT	GAT	GAT	TGT	GGT	GAT	GGA	AGT	GAT	GAA	ATG	AAC	TGT	GCT	GAT
Gly	Ile	Asp 130	Asp	Cys	Gly	Asp	Gly 135	Ser	Asp	Glu	Met	Asn 140	Cys	Ala	Asp
GAT 479	GAA	GTG	ATA	ACA	TCA	ATA	AAT	GGT	AAC	GAA	TCA	ATC	AAT	ATC	AGA
Asp	Glu 145	Val	Ile	Thr	Ser	Ile 150	Asn	Gly	Asn	Glu	Ser 155	Ile	Asn	Ile	Arg
TGT 527	GAT	CCG	GAT	CAA	TTT	CGA	TGT	GAA	AAT	GGA	AAA	TGT	ATC	GCA	CAA
Cys 160	Asp	Pro	Asp	Gln	Phe 165	Arg	Cys	Glu	Asn	Gly 170	Lys	Cys	Ile	Ala	Gln 175
ATT 575	GAT	CGA	TGT	AAT	CGA	AAA	TAT	GAT	TGT	GAT	GAT	GGT	ACA	GAT	GAA
Ile	Asp	Arg	Cys	Asn 180	Arg	Lys	Tyr	Asp	Cys 185	Asp	Asp	Gly	Thr	Asp 190	Glu
ACA 623	ACT	TGT	GAA	TAT	TTC	GTG	CAA	GCT	TTG	CAA	CAA	GCG	AGA	GGT	GTA

Thr Thr Cys Glu Tyr Phe Val Gln Ala Leu Gln Gln Ala Arg Gly Val
 195 200 205
 ACG GTG CAG GAT AAT GCA ATT CGA GAT GAC GAG ATA CCA AAT TAT ACT
 671
 Thr Val Gln Asp Asn Ala Ile Arg Asp Asp Glu Ile Pro Asn Tyr Thr
 210 215 220
 GTA TCC ATG GAA CAG AAA TAC GAT CAA GTA AAG GAA GAT AAG GAG CGG
 719
 Val Ser Met Glu Gln Lys Tyr Asp Gln Val Lys Glu Asp Lys Glu Arg
 225 230 235
 CGA ATG CAA GAG GAG GAG GAA CAG GAA AGG CTG AGA GAG TAC GAG GAA
 767
 Arg Met Gln Glu Glu Glu Gln Glu Arg Leu Arg Glu Tyr Glu Glu
 240 245 250 255
 CAG ATA CAG GAA AAA TTG AGG CAG GAG GAA GAA AGA GAA CGG CAA GAA
 815
 Gln Ile Gln Glu Lys Leu Arg Gln Glu Glu Glu Arg Glu Arg Gln Glu
 260 265 270
 CAG GAA AGA AGA CAA AAG GAA CGA GAA AGA ATG GAA CAA GAA AGG ATA
 863
 Gln Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile
 275 280 285
 AGA CAA GAA TAT GAT GAA AAG GAA AGA CAA AGG CAA TAT GCT GAA CAG
 911
 Arg Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln
 290 295 300
 GC
 913

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Leu Asn Ser Arg Ile Ser Gly Val His Arg Asn Thr Ala Gly Ala
 1 5 10 15
 Leu Gln Arg Phe Ala Leu Asn Gly Gln Asn Thr Leu Asn Glu Gly Ser
 20 25 30
 Ser Tyr Glu Pro Asn Gly Leu Phe Val Phe Ser Ala Ile Asn Gly Ser
 35 40 45
 His Thr Asp Ser Leu Ser Gln Tyr Gly Glu Gly Ile Asn Glu Asn Tyr
 50 55 60
 His Ser Gly Thr Asn Tyr Tyr Asp Glu Val Glu Leu Arg Asp Lys Thr

65	70	75	80
Asn Gln Thr Ser Tyr Ile Asn Gly Asn Asp Asn Gly Ile Asn Gly Lys	85	90	95
Asp Asp Glu Asp Leu Asp Glu Cys Ser Asp Gln Glu Phe Arg Cys Pro	100	105	110
Tyr Leu Ala Lys Thr Leu Cys Val His Tyr Leu Lys Ile Cys Asp Gly	115	120	125
Ile Asp Asp Cys Gly Asp Gly Ser Asp Glu Met Asn Cys Ala Asp Asp	130	135	140
Glu Val Ile Thr Ser Ile Asn Gly Asn Glu Ser Ile Asn Ile Arg Cys	145	150	155
Asp Pro Asp Gln Phe Arg Cys Glu Asn Gly Lys Cys Ile Ala Gln Ile	165	170	175
Asp Arg Cys Asn Arg Lys Tyr Asp Cys Asp Asp Gly Thr Asp Glu Thr	180	185	190
Thr Cys Glu Tyr Phe Val Gln Ala Leu Gln Gln Ala Arg Gly Val Thr	195	200	205
Val Gln Asp Asn Ala Ile Arg Asp Asp Glu Ile Pro Asn Tyr Thr Val	210	215	220
Ser Met Glu Gln Lys Tyr Asp Gln Val Lys Glu Asp Lys Glu Arg Arg	225	230	235
Met Gln Glu Glu Glu Glu Gln Glu Arg Leu Arg Glu Tyr Glu Glu Gln	245	250	255
Ile Gln Glu Lys Leu Arg Gln Glu Glu Glu Arg Glu Arg Gln Glu Gln	260	265	270
Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile Arg	275	280	285
Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln	290	295	300

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..626

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR

(B) LOCATION: 627..1016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GT TTT GTT GTA CTA CTC GTT GTT GCA ATA TGG ATT GAA ATG AGC CAA
47
  Phe Val Val Leu Leu Val Val Ala Ile Trp Ile Glu Met Ser Gln
    1             5             10             15

GGC CAA CAA ATG ATC AAA CAA TGT AAA TGT TCT GAT ATT GCA CCA TGT
95
Gly Gln Gln Met Ile Lys Gln Cys Lys Cys Ser Asp Ile Ala Pro Cys
                20             25             30

CAA TTA ACT GCC GTT CAA TCA GTT TTA CCA TGT GCT GAT CAA TGC CAG
143
Gln Leu Thr Ala Val Gln Ser Val Leu Pro Cys Ala Asp Gln Cys Gln
                35             40             45

AAA TAT ATT ACT TCA ATT GGT GGT AAT TAT GAT CAA ATT AGT AAC TGT
191
Lys Tyr Ile Thr Ser Ile Gly Gly Asn Tyr Asp Gln Ile Ser Asn Cys
                50             55             60

TTT AAA CAG AAA CAA TCA ATT ATA AAT GAT GCT ATG AAA TGT GCT CAA
239
Phe Lys Gln Lys Gln Ser Ile Ile Asn Asp Ala Met Lys Cys Ala Gln
    65             70             75

GAT GCT TTC CCA AAT GCA TGC GCA CAA GGT GAA CCA AAA ATG GTA CCA
287
Asp Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys Met Val Pro
    80             85             90             95

AAA CGA TTC GGA AAA GGT CTT CAA TTA GCT GTA ATG ACT GAT ATC AAC
335
Lys Arg Phe Gly Lys Gly Leu Gln Leu Ala Val Met Thr Asp Ile Asn
                100             105             110

AAA GAA TTA CAA CGA ATG GGA ATA GCA AAT CAA GTT ACT CAA CTA ATC
383
Lys Glu Leu Gln Arg Met Gly Ile Ala Asn Gln Val Thr Gln Leu Ile
                115             120             125

TCC CAA GGT CGA CGA TTC TTT AAA TGC TTC CAA TCG TGT ATG ATG AAA
431
Ser Gln Gly Arg Arg Phe Phe Lys Cys Phe Gln Ser Cys Met Met Lys
                130             135             140

AAA TTG GGC TCA TGT TCT CCA GAT TGT GGT CTT GAT TTA CCA TCT GAT
479
Lys Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp
    145             150             155

AAT GTT ATG GTT CAA ACA GTT AAA AAT TGC GCT CAA AAA AGT GGT ATT
527
Asn Val Met Val Gln Thr Val Lys Asn Cys Ala Gln Lys Ser Gly Ile
    160             165             170             175

CAA ACT GCA TCG GTG CAA GAT CTT TGC TTT TGC GTC GAA CAA GCT GGT
```

575
 Gln Thr Ala Ser Val Gln Asp Leu Cys Phe Cys Val Glu Gln Ala Gly
 180 185 190

ATT CGG CAA CTT TCT GAT GTA TGT CCT CGT ATA CAA ATT TTC AAA ACG
 623
 Ile Arg Gln Leu Ser Asp Val Cys Pro Arg Ile Gln Ile Phe Lys Thr
 195 200 205

AAA TGAGTATTGA GAATATTGCA CTAGCAGCAA TCATTATTTT TCTCGAGAAT
 676
 Lys

TTTCGCTATC AATAAGTTGG AATATGATTA CAATAATATA TATATTAAC TCAAAAAATCT
 736

TTCTTCTTCA AAATTATTTT TCATTTCGCT CTCATAATTG CATGATAATA GTCATAATGA
 796

AAAACAGGTT TTCTTTTTTT AAAATGATAA CTTCAAACAA ATAGGTATTT CTTGATATAT
 856

ATATGTATGT ATGTATGTGT GTGTGTGTGT GTGTGTGTAT GTGTGTGTTT GTGTATGTGT
 916

ATATGTATGT ATGTATGTAT GTATGTATGT ATGTGTAGGA GAAAAGCAAA CTAAACAGTA
 976

AATGAAAGAA AAAAATAAGT CAAATAAAAG TTTGATAATT
 1016

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe	Val	Val	Leu	Leu	Val	Val	Ala	Ile	Trp	Ile	Glu	Met	Ser	Gln	Gly	1	5	10	15
Gln	Gln	Met	Ile	Lys	Gln	Cys	Lys	Cys	Ser	Asp	Ile	Ala	Pro	Cys	Gln	20	25	30	
Leu	Thr	Ala	Val	Gln	Ser	Val	Leu	Pro	Cys	Ala	Asp	Gln	Cys	Gln	Lys	35	40	45	
Tyr	Ile	Thr	Ser	Ile	Gly	Gly	Asn	Tyr	Asp	Gln	Ile	Ser	Asn	Cys	Phe	50	55	60	
Lys	Gln	Lys	Gln	Ser	Ile	Ile	Asn	Asp	Ala	Met	Lys	Cys	Ala	Gln	Asp	65	70	75	80
Ala	Phe	Pro	Asn	Ala	Cys	Ala	Gln	Gly	Glu	Pro	Lys	Met	Val	Pro	Lys	85	90	95	

Arg	Phe	Gly	Lys	Gly	Leu	Gln	Leu	Ala	Val	Met	Thr	Asp	Ile	Asn	Lys
			100					105					110		
Glu	Leu	Gln	Arg	Met	Gly	Ile	Ala	Asn	Gln	Val	Thr	Gln	Leu	Ile	Ser
		115					120					125			
Gln	Gly	Arg	Arg	Phe	Phe	Lys	Cys	Phe	Gln	Ser	Cys	Met	Met	Lys	Lys
		130				135					140				
Leu	Gly	Ser	Cys	Ser	Pro	Asp	Cys	Gly	Leu	Asp	Leu	Pro	Ser	Asp	Asn
145					150					155					160
Val	Met	Val	Gln	Thr	Val	Lys	Asn	Cys	Ala	Gln	Lys	Ser	Gly	Ile	Gln
				165					170					175	
Thr	Ala	Ser	Val	Gln	Asp	Leu	Cys	Phe	Cys	Val	Glu	Gln	Ala	Gly	Ile
			180					185					190		
Arg	Gln	Leu	Ser	Asp	Val	Cys	Pro	Arg	Ile	Gln	Ile	Phe	Lys	Thr	Lys
		195				200						205			

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu
1				5				

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Gln	Asp	Ala	Phe	Pro	Asn	Ala	Cys	Ala	Gln	Gly	Glu	Pro	Lys
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Ile Ala Pro Cys Gln Leu Thr Ala Val Gln Ser Val Leu Pro Cys
1 5 10 15
Ala Asp Gln Cys Gln Lys
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Gly Ser Cys Ser Pro Asp Cys Gly Leu Asp Leu Pro Ser Asp Asn
1 5 10 15
Val Met Val Gln Asp Val
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGATCCCG AGTTAAATAG TCG
23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCAGGATCC TGCACCG
17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGAGAGAGA GAGAGAGAGA ACTAGTCTCG AGTTTTTTTT TTTTTTTTTT
50

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGYTCNCNG AYTGYGG
17

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /label= PRIMER
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGYAGTCCNG AYTGYGG
17

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /label= PROBE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGNACCATNA CRTTRTC
17

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..27
 - (D) OTHER INFORMATION: /label= PROBE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGTTTGAAC CATAACATTA CAGATGG
27

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTGCAATAT GGGATCCAAT GAGCC
25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /label= PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCTAGTGCA GGATCCTCAA TACTC
25